

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

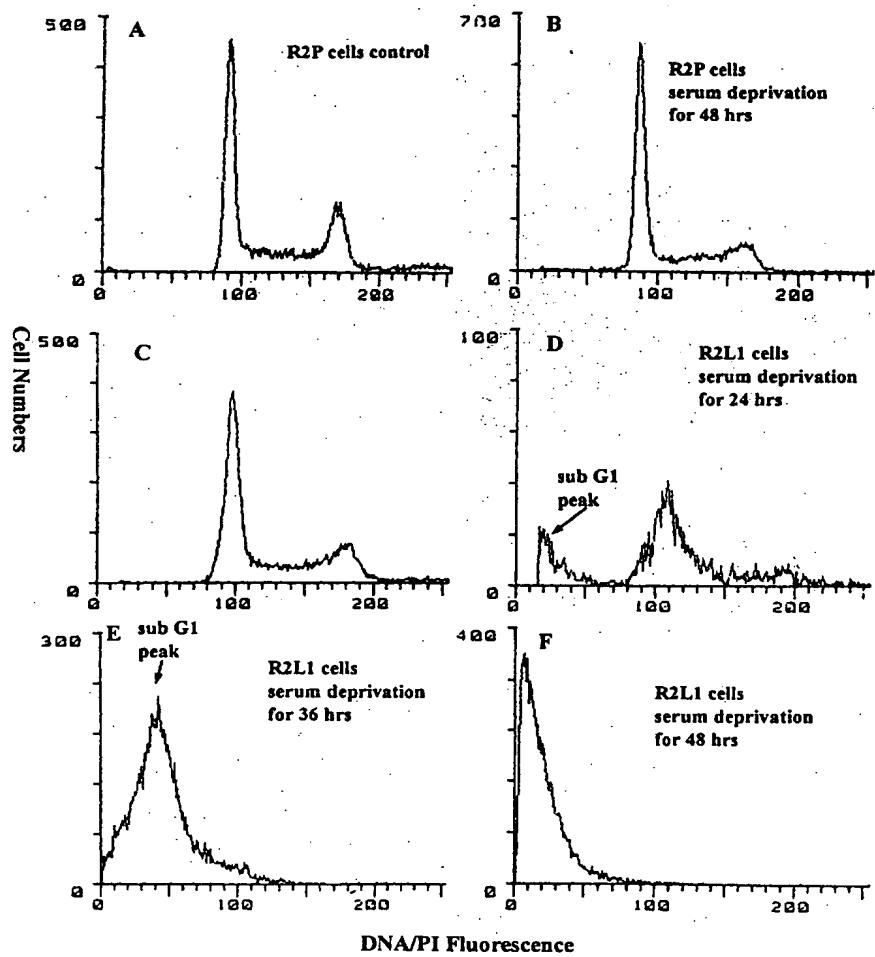
**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

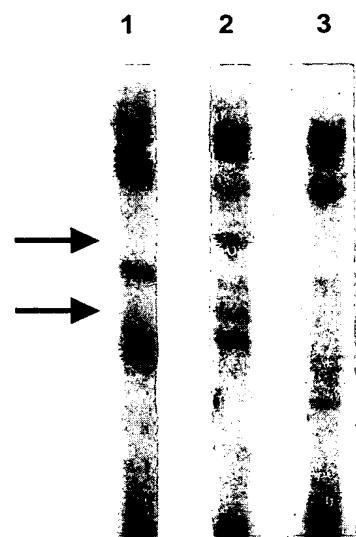
**Figure 1**



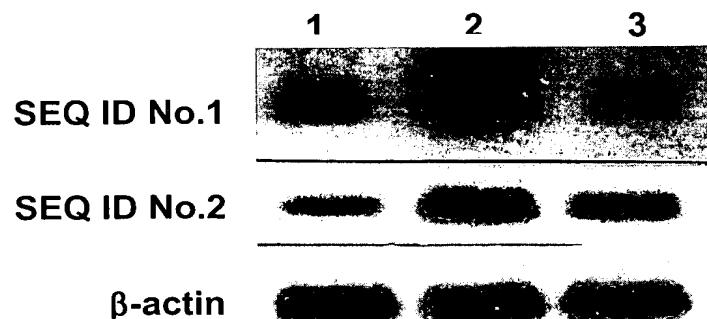
**Figure 2**



**Figure 3**



**Figure 4**



## Figure 5

### DNA Sequence of ARBP cDNA (SEQ ID No. 3) and predicted amino acid sequence of encoded protein (SEQ ID No. 4)

GCTGGCCGGGTGACCGCTGGTGTCACTCGTTAGGAAGCGGCTTCACCGCCAACAGCACGGCC  
1 Met Ala Gly Ala Leu Val Arg Lys Ala Ala Asp Tyr Val Arg Ser Lys Asp Phe Arg Asp  
ATG GCT GGA GCT CTG GTG CGC AAA GCA GCG GAC TAT GTC CGG AGC AAG GAC TTC CGG GAC  
21 Tyr Leu Met Ser Thr His Phe Trp Gly Pro Val Ala Asn Trp Gly Leu Pro Ile Ala Ala  
TAT CTC ATG AGT ACG CAC TTC TGG GGC CCA GTT GCC AAC TGG GGT CTC CCC ATT GCT GCT  
41 Ile Asn Asp Met Lys Lys Ser Pro Glu Ile Ile Ser Gly Arg Met Thr Phe Ala Leu Cys  
  
ATC AAT GAC ATG AAG AAA TCT CCA GAG ATT ATC AGT GGG CGG ATG ACT TTC GCC CTC TGT  
61 Cys Tyr Ser Leu Thr Phe Met Arg Phe Ala Tyr Lys Val Gln Pro Arg Asn Trp Leu Leu  
TGC TAT TCT CTG ACA TTC ATG AGA TTT GCC TAC AAG GTA CAA CCC CGA AAC TGG CTT CTG  
81 Phe Ala Cys His Val Thr Asn Glu Val Ala Gln Leu Ile Gln Gly Gly Arg Leu Ile Asn  
TTT GCG TGC CAT GTG ACA AAC GAA GTC GCT CAG CTC ATT CAG GGA GGA CGA CTT ATC AAC  
101 Tyr Glu Met Ser Lys Arg Pro Ser Ala \*  
TAC GAG ATG AGT AAG CGG CCA TCT GCC TAG  
CAGTGCAAGGACCAGCTCTTGAAAGGGACAGTGCT  
CCAGCCACTGTTGCCAACAGATCACGTCAAGCATGAATAGTCGTGCTGAGGGAAAACACGGAAGACTATCTTAATGACCATG  
CCAACATTATTGAATAGCCAAGAATCCCCAAACCAACTCTCGGCTGCCTTATCAATGCTAAACTTATTGTCTTCATCAGGAGT  
AGTTCAAAATATGCAGCTAATTAAATAATTGAAATGATGTTATCTATAGCAATCTGTAGTAATATGTATATTATCTATTGGGAT  
TTGTGTAATAAAAATCTAAGGGAACAAAACCTTATAACTACAAGCACTTAAGCCTCAAAATTCTGACTTTCTTAATGAC  
TATAGTATAACCCTCAGTTGGTCACATGTCTACACATAATTCCAGTGATAACAAGTAGCGGTGTTCCATATGTAATTCAAGAT  
CTGAACCTTAATGGCAATAATGGTTAAATATTGCGAAAAAAAAAAA

**Figure 6**

Sequence 1: human 102 aa  
Sequence 2: rat 109 aa  
Sequence 3: mouse 109 aa

Sequences (1:2) Aligned. Score: 97.0588  
Sequences (1:3) Aligned. Score: 96.0784  
Sequences (2:2) Aligned. Score: 100  
Sequences (2:3) Aligned. Score: 99.0826  
Sequences (3:2) Aligned. Score: 99.0826  
Sequences (3:3) Aligned. Score: 100

rat MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKSPEIISGRMTFALC  
mouse MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKSPEIISGRMTFALC  
human MAGALVRKAADYVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKSPEIISGRMTFALC  
\*\*\*\*\*  
rat CYSLTTFMRFAYKVQPRNWLLFACHVTNEVAQLIQGGRLINYEMSKRPSA  
mouse CYSQTFMRFAYKVQPRNWLLFACHVTNEVAQLIQGGRLINYEMSKRPSA  
human CYSLTTFMRFAYKVQPRNWLLFACHATNEVAQLIQGGRLIKHE-----  
\*\*\* \*\*\*\*\*: ;\*

**Figure 7**

QUERY IS SEQ ID. NO. 3, SUBJECT IS HUMAN

Homo sapiens NM\_016098, mRNA  
Length = 988

Score = 361 bits (182), Expect = 1e-96  
Identities = 284/318 (89%)  
Strand = Plus / Plus

Query: 56 gcacggccatggctggagcttgcgaaaggcagcgactatgtccggagaaggact 115  
Sbjct: 115 gcacaggccatggccggacacattttatcacaaaaaggcggccggactatgtccggaaaccaggatt 174

Query: 116 tccgggactatctcatgagtacgcacttctggggccagttgccaactgggtctcccc 175  
||||||| ||||| ||||| |||||  
Sbjct: 175 tccgggactacctcatgagtacgcacttctggggccagttgccaactgggtctcccc 234

Query: 176 ttgcgttatcaatgacatgaagaaatctccagagattatcagtggcgatgactttcg 235  
||||||| ||||| ||||| |||||  
Sblast: 235 ttgcgttatcaatgatatatgaaaaaaatctccagagattatcagtggcgatgacatgg 294

Query: 236 ccctctgttgcattctctgacattcatgagattgcctacaaggtaacaaccccgaaact 295  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 356 ttatcaactacgagatga 373

Sbjct: 415 ttatcaaacacgagatga 432

Identities = 31/32 (96%)  
Strand = Plus / Plus

Query: 857 aacttaatggcaataaatggtttaaatattt 888  
          ||||||| ||||| ||||| |||||  
Sbjct: 926 aacttaatggcaataaatgatttaaatattt 957

Score = 46.1 bits (23), Expect = 0.092  
Identities = 32/35 (91%)  
Strand = Plus / Plus

Query: 595 gagtagttcaaaatatatgcagctaattataattt 629  
          ||||||| ||||||| ||||||| |||||||  
Sbjct: 660 gagtagctcaaaatatatgcattaattataattt 694

Score = 44.1 bits (22), Expect = 0.36  
Identities = 95/118 (80%), Gaps = 1/118 (0%)  
Strand = Plus / Plus

Query: 651 atctgttagtaatatgtatattatctattggatttgtgtataaaaaatctaaggaaaca 710  
          ||||||| ||||||| ||||| ||||| | ||||| ||||| |||||  
Sbjct: 708 atctgcacttagtataatcatctattagaattttacttaatgaaaaactgaaagaaaaca 767

**Figure 8**

QUERY IS SEQ ID NO. 3, SUBJECT IS MOUSE  
Mus musculus adult male kidney cDNA, RIKEN full-length enriched library,  
clone:0610007A16 product:brain protein 44-like, full insert sequence  
Length = 886  
Score = 1374 bits (693), Expect = 0.0  
Identities = 833/875 (95%), Gaps = 6/875 (0%)  
Strand = Plus / Plus

Query: 19 ggtgtcatccgtttaggaagcggcttacccccaacacgcacggccatggctggagctctg 78  
Sbjct: 13 ggtgtcatctgtctaggtagcggtttacccccaacggcacggccatggctggagcgctg 72

Query: 79 gtgcgcaaagcagcgactatgtccggagaaggacttccggactatctcatgagtaacg 138  
Sbjct: 73 gtgcgcaaagcgccggactatgtccggagaaggacttccggactatctcatgagtaacg 132

Query: 139 cacttctggggcccagttgccaactgggtctccccattgtctatcaatgacatgaag 198  
Sbjct: 133 cacttctggggcccagttgccaactgggtctccccattgtctatcaatgacatgaag 192

Query: 199 aaatctccagagattatcagtggcgatgactttcgccctgttgcatttcgtaca 258  
Sbjct: 193 aaatctccagagattatcagtggcgatgactttcgccctgttgcatttcgtaca 252

Query: 259 ttcatgagattgcctacaaggtacaaccccgaaactgggtctgtttgcgtgcattgt 318  
Sbjct: 253 ttcatgagattgcctacaaggtacaacctcgaaactgggtttgttgcattgt 312

Query: 319 acaaacgaagtgcgtcagctattcaggaggacgacttatcaactacgagatgagtaag 378  
Sbjct: 313 acaaacgaagtgcgtcagctattcaggaggacgacttatcaactacgagatgagtaag 372

Query: 379 cggccatctgccttagcagtgcaggaccaggcttggaaaggacagtgtccaggccatg 438  
Sbjct: 373 cggccatctgcgtacaaggaccaggcttggaaaggacagtgtccaggccatg 432

Query: 439 ttgcggccacagatcacgtcagcatgaatagtgcgtgtggaaaacacggaaacta 498  
Sbjct: 433 ctgcagccacagatcatgtcagcatgagtagtgcgtgtggaaaacacagaatgcta 492

Query: 499 tcttaatgaccatgccaacattattgaatagccaagaatccccaaaccaactctcggt 558  
Sbjct: 493 tc-ttaatgaccatgccaacattattgaatagccgagagtccctaaacccactctctgt 551

Query: 559 gccttatcaatgctaaacttttgcgttcatcaggagtagttcaaatatgcagctaa 618  
Sbjct: 552 gccttatcaatgctaaaccttattgttgcgttcatcaagagtagttcaaatatgcactaa 611

Query: 619 tttaataatttgaatgtg---ttatctatagcaatctgttagtaatatgttatattct 675  
Sbjct: 612 tttaataatttgaatgtggtttatctatagcaatctgttagtaatatgttatattct 671

Query: 676 attgggatttgcgtataaaaaatctaaggacaaaactttataactacaagcacttaa 735  
Sbjct: 672 attgggatttgcgtataaaaaatctaaggacaaaatttataactacaagcacttaa 731

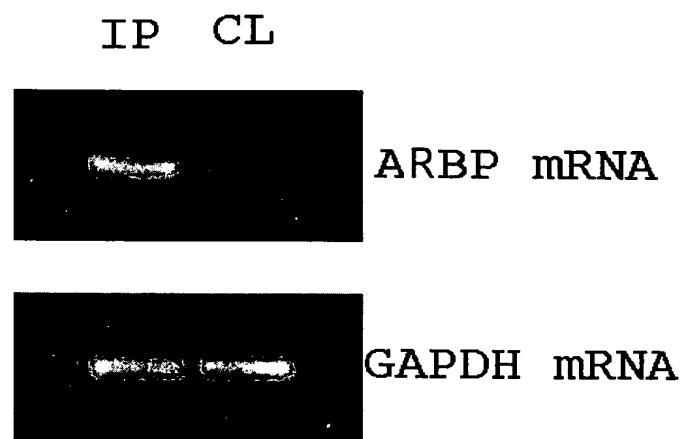
Query: 736 gtcctcaaaattcttgactttttttatgactatagttataaccctcagttggtcacat 795  
Sbjct: 732 gtactcaaaattcttgactttttttatgactatgacaatagta-aaccctcagttggtcacat 790

Query: 796 gtctacacataattccagtgataacaagtagcggtgtttccatatgttaattcagatct 855  
Sbjct: 791 gtctacacataattccagtgataacaagtagtgcgtgtttccatatgttaactcagatct 850

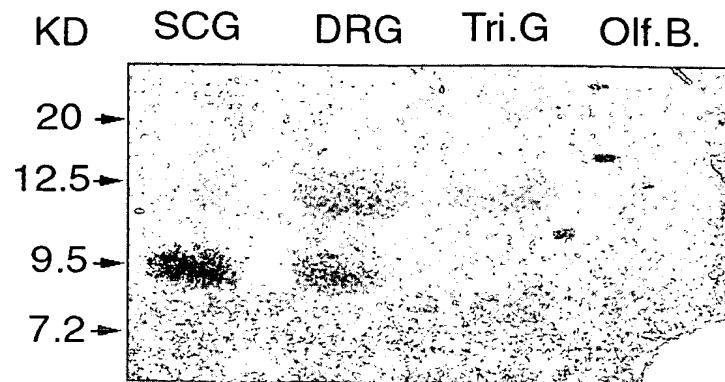
Query: 856 g-aacttaatggcaataaaatggttaaatattgc 889  
Sbjct: 851 gtaacttaatggcaataaaatggttaaatattgc 885

**Figure 9**

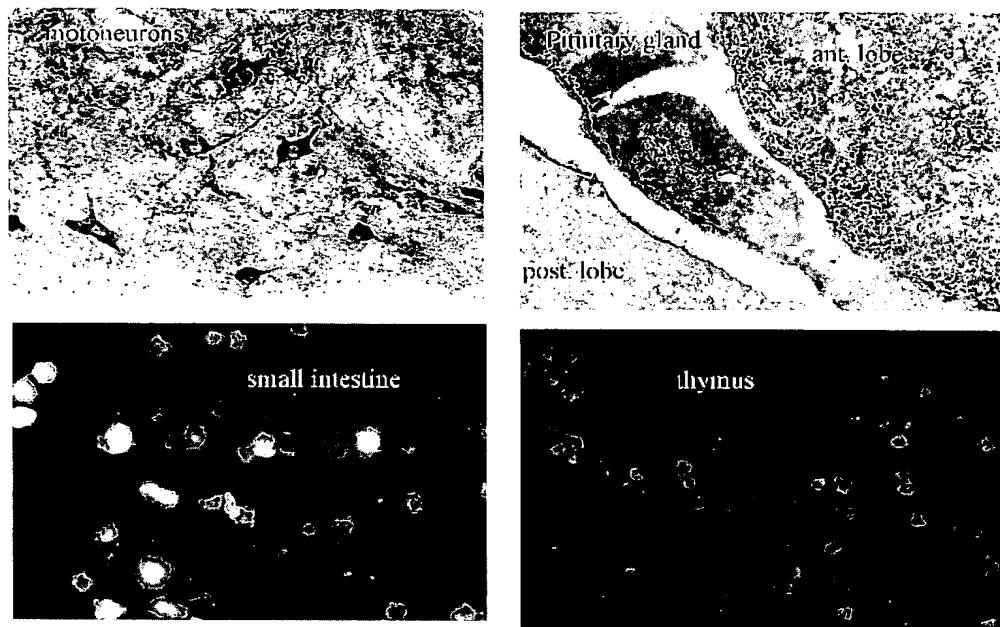
**Figure 10**



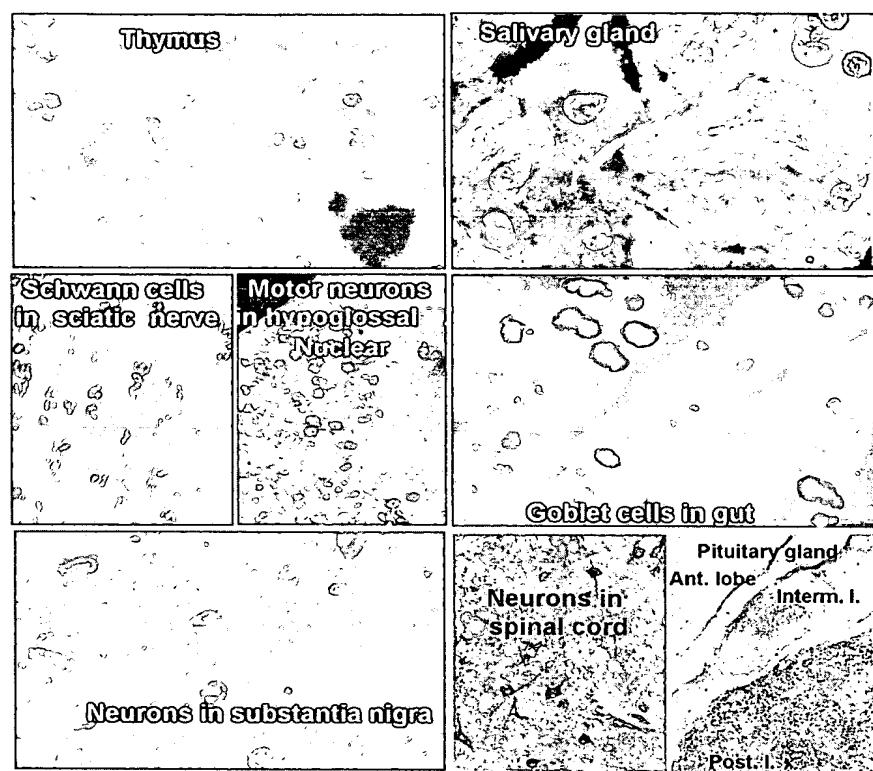
**Figure 11**



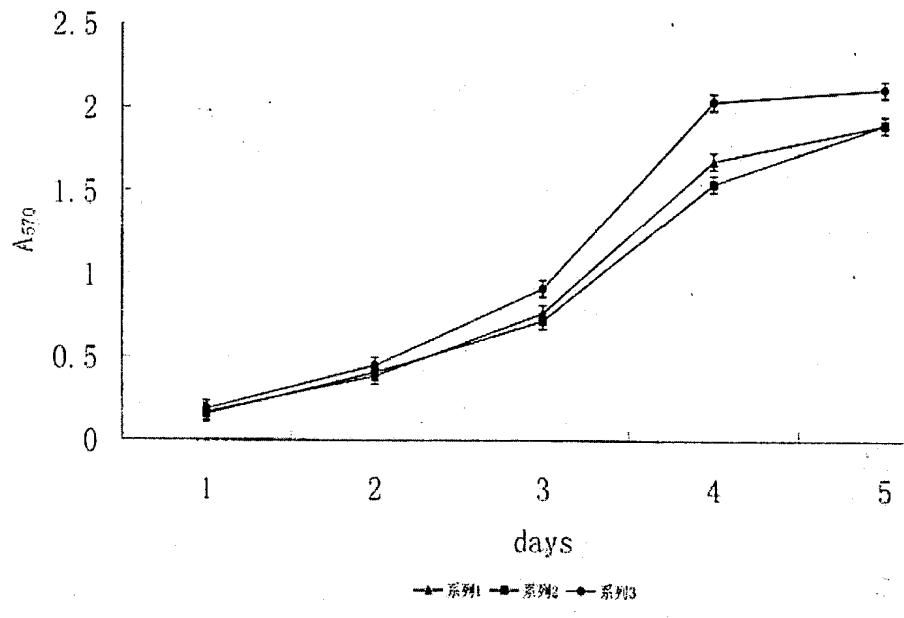
**Figure 12**



**Figure 13**



**Figure 14**



**Figure 15**

